

### ***Amendments***

#### ***In the Specification:***

On page 22, line 27, delete "Bestfit" and insert therefor --Bestfit®--.

On page 23, line 1, delete "Bestfit" and insert therefor --Bestfit®--.

On page 23, line 3, delete "Bestfit" and insert therefor --Bestfit®--.

On page 38, line 16, delete "Bestfit" and insert therefor --Bestfit®--.

On page 38, line 18, delete "Bestfit" and insert therefor --Bestfit®--.

#### ***In the Claims:***

Please amend the following claims:

*Sub E6*  
D 7 95. An isolated polynucleotide comprising a nucleotide sequence encoding an amino acid sequence at least 95% identical to amino acids 1 to 260 of SEQ ID NO:42;

wherein % identity is determined using the [Bestfit] Bestfit® program with parameters that calculate % identity over the full length of amino acids 1 to 260 of SEQ ID NO:42 and that allow gaps of up to 5% of the total number of amino acid residues in amino acids 1 to 260 of SEQ ID NO:42.

*Sub E1*  
D 2 98. The isolated polynucleotide of claim 95, wherein said amino acid sequence is at least 95% identical to amino acids 1 to 488 of SEQ ID NO:42;

wherein % identity is determined using the [Bestfit] Bestfit® program with parameters that calculate % identity over the full length of amino acids 1 to 488 of SEQ ID NO:42 and that allow

Sub E7  
D2  
cont

gaps of up to 5% of the total number of amino acid residues in amino acids 1 to 488 of SEQ ID NO:42.

Sub E8  
D3

101. The isolated polynucleotide of claim 98, wherein said amino acid sequence is at least 95% identical to amino acids -17 to 488 of SEQ ID NO:42;

wherein % identity is determined using the [Bestfit] Bestfit<sup>®</sup> program with parameters that calculate % identity over the full length of amino acids -17 to 488 of SEQ ID NO:42 and that allow gaps of up to 5% of the total number of amino acid residues in amino acids -17 to 488 of SEQ ID NO:42.

Sub E9  
D4

104. The isolated polynucleotide of claim 101, wherein said amino acid sequence is at least 95% identical to amino acids -18 to 488 of SEQ ID NO:42;

wherein % identity is determined using the [Bestfit] Bestfit<sup>®</sup> program with parameters that calculate % identity over the full length of amino acids -18 to 488 of SEQ ID NO:42 and that allow gaps of up to 5% of the total number of amino acid residues in amino acids -18 to 488 of SEQ ID NO:42.

Sub E10  
D5

115. An isolated polynucleotide comprising a nucleotide sequence encoding an amino acid sequence at least 95% identical to the mature amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642,

wherein % identity is determined using the [Bestfit] Bestfit<sup>®</sup> program with parameters that calculate % identity over the full length of the mature amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642 and that allow gaps of up to 5% of the total number of amino

*Sub DS  
E10  
cont*  
acid residues of the mature amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642.

*Sub E11*  
117. The isolated polynucleotide of claim 115, wherein said amino acid sequence is at least 95% identical to the complete amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642;

*DB*  
wherein % identity is determined using the [Bestfit] Bestfit® program with parameters that calculate % identity over the full length of the complete amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642 and that allow gaps of up to 5% of the total number of amino acid residues of the complete amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642.

*Sub G7*  
127. An isolated polynucleotide comprising a first polynucleotide which hybridizes to a second polynucleotide, wherein the second polynucleotide consists [consisting] of the nucleotide sequence of the coding region of SEQ ID NO:41, or the full-length complement thereof, under conditions comprising:

*D7*  
(a) incubating overnight at 42°C in a solution consisting of 50% formamide, 5x SSC, 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA; and

(b) washing at 65°C in a solution consisting of 0.1x SSC;  
wherein said first polynucleotide is at least 70 nucleotides in length.